

Enhance the Accuracy of Pneumonia Detection Using Feature Fusion and Artificial Intelligence

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Abstract—Pneumonia is a deadly bacterial infection that affects the lungs in the human body. According to the World Health Organization (WHO), pneumonia causes one out of three mortalities in India. Chest X-ray (CXR) images are utilized to diagnose pneumonia and it must be examined by a professional radiotherapist. Thus, developing an autonomous system for identifying pneumonia would be beneficial for prompt treatment. In this research, we used Artificial Intelligence (AI) and feature fusion methods to identify pneumonia from CXR images. The images are collected from Kaggle and processed for resizing, noise removal, and data balancing. The processed images are given to Deep Learning (DL) models like Inception and Xception to extract the features. Then, Canonical Correlation Analysis (CCA) is employed to fuse the features obtained from both DL models. The Inception, Xception, and fused features are given to Machine Learning (ML) models such as Support Vector Machine (SVM) and Bayesian Logistic Regression (BLR) for pneumonia classification. Finally, each feature with the ML model is evaluated individually using metrics such as accuracy, specificity, recall, precision, and F1 score. The experimental outcome shows that the CCA fused features with BLR outperform the other combinations, achieving the highest accuracy of 98.91%.

Keywords—Pneumonia, Chest X-Ray, Medical Images, Accuracy, Feature Selection, Artificial Intelligence

Introduction

Pneumonia is an inflammation of the lung parenchyma that is frequently caused by pathogenic bacteria, physical and chemical factors, immunological damage, and various drugs [1]. Pneumonia kills almost 2,200 children under the age of five every day, accounting for more than 800,000 deaths annually. More than 1,400 out of 100,000 children will develop pneumonia. According to the 2014 Global Burden of Disease Study [2], the leading cause of death in the respiratory tract was pneumonia. Approximately 35% of European hospitalized patients and 27.3% of people globally are affected by pneumonia. The Johns Hopkins Bloomberg School of Public Health reports that pneumonia is the top killer of Indian children younger than five years old [3]. In 2015, around 297,000 people died from pneumonia and diarrhea. Additionally, in 2015, pneumonia was the leading cause of death for children under five. Furthermore, pneumonia is more common in elderly persons (65 and older), with a fatality rate that is directly proportional to age. The rising number of infant pneumonia deaths has motivated scientists throughout the world to propose faster and more accurate approaches to detect the disease. The most prevalent and useful methods are radiology-based, and as technology progresses, more measures are developed. Among the various diagnostic radiological techniques used to diagnose pulmonary disease, computed tomography (CT), magnetic resonance imaging (MRI), and computed x-ray imaging (CXR) are the most cost-effective and practical options due to their portability, ease of use in hospitals, and lower radioactive doses to patients [4].

Even highly skilled medical personnel find it difficult to detect pneumonia using X-ray images because these images can

provide identical regional information in cases of other diseases, such as lung cancer [5]. Therefore, traditional methods of diagnosing pneumonia are arduous and time-consuming, and there is no standardized approach for determining if a patient has pneumonia.

In this research, automated classification of pneumonia from CXR images is performed. To achieve a better recognition rate, the CCA method is employed to obtain fused features from the Inception and Xception models. ML models such as SVM and BLR are chosen to classify pneumonia and normal images. Finally, the best model is identified through performance evaluation.

Related Works

Several academics have recently published several AI-based solutions for various health issues. The study [6] aims to create a system that can accurately detect and categorize pneumonia cases using Naive Bayesian (NB) and Random Forest (RF). The model was trained on CXR samples from pneumonia patients using a hash-based method to reduce classification errors and improve detection accuracy. To apply a future scaling technique that improved the model's performance, the target variable's categorical labels were encoded using a hash encoding strategy. Tested the approaches with a variety of fine-tuned hyper-parameter values and compared their accuracy and error. The NB produces a high accuracy rate with a low error value. In a study [7], the author used k-Nearest Neighbors (k-NN) and Multilayer Perceptron (MLP) on pre-processed CXR images to identify pneumonia. Equalization, Mask R-Network, and Otsu thresholding were applied to the CXR images. The textural features were then stripped from the CXR images before being transmitted to the classification algorithms. Then the Over-sampling method is used to correct the class imbalance in the training sample. In all metrics examined, the MLP method outperformed the k-NN strategy.

The article [8] describes a novel kNN-SVM approach for diagnosing COVID-induced pneumonia using CXR images. Computed the features by applying Transfer Learning (TL) to the traditional VGG16 model. The dimensionality reduction approach then employs the autoencoder algorithm. The three targets pneumonia, healthy, and COVID, are finally identified using a new kNN-regularized SVM algorithm. According to comprehensive experimental data, the recommended kNN-SVM outperforms radiologists in detecting COVID-19-induced pneumonia from CXR. In the paper [9], a novel strategy is presented to utilize patients' CXR images to predict the likelihood of lung illness. The framework includes dataset acquisition, image enhancement, ROI estimation, feature extraction, and disease identification. Two publicly available CXR image datasets are used. Using morphological techniques and dynamic area selection based on intensity values of pixels, a modified region growth technique was created for accurate ROI extraction of chest areas. Visual, form, texture, and intensity features were retrieved from all of the ROI images. The soft computing techniques used in this application include Artificial Neural Networks (ANNs), SVM, KNN, and Ensemble Classifiers. The usage of recurrent neural networks (RNNs) with long short-term memory (LSTM) has been proposed as a DL architecture for accurate lung disease diagnosis. Experimental findings demonstrate the proposed algorithm's robustness and efficiency when compared with state-of-the-art techniques.

The article [10] introduces Ensemble Learning (EL) for automatic detection of pneumonia using CXR images. The foundation of the technique is the Convolutional Neural Network (CNN). These models have been utilized to enhance the performance of numerous medical activities, rather than training CNN models from the start. Pretrained three popular CNNs are recommended from the ImageNet database: DenseNet169, MobileNetV2, and Vision Transformer. These models are fine-tuned while training on the CXR dataset. The final step in the experimental phase is to merge the features collected from all three models to obtain the results. In terms of testing performance, the suggested EL method outperforms current research approaches. The study [11] aimed at categorizing pneumonia from CXR images. The dataset used in this study has two basic categories: normal and pneumonia. The project aims to develop a model for automatically classifying pneumonia using X-ray images. The categorization strategy in this work is based on the CNN approach. The choice of CNNs for classification in this study is justified since these networks can extract features automatically, avoiding the requirement for input data preparation while still producing high-quality features and reliable classification results. The created CNN model worked well in the pneumonia classification task. The research [12] aims to develop a lightweight, portable, and reliable model that can help in the identification of pneumonia. Three independent models with different kernel sizes were combined to construct a CNN architecture. A novel weighted ensemble technique was used to integrate the results of various models. This method gives a threshold that can be adjusted to change the detection abilities of the model. By adjusting the weighting of each model's output using the adjustable threshold value, the classification result may change. Because it does not require deep neural networks or TL, the model is lightweight and suitable for diagnostic

purposes.

Materials and Methods

For pneumonia detection, normal and pneumonia-affected CXR images are collected. The required pre-processing is done to ensure the quality of the input data. The processed images are then given to Inception and Xception networks to extract the features. The features obtained by the two models are combined using the canonical correlation analysis (CCA) algorithm. ML models such as SVM and BLR are used to classify the pneumonia and normal CXR images. The features from Inception, Xception, and CCA are given to the models. The performance of the two ML models on three different feature sets is evaluated using performance measures. The data collection and processing are detailed in this section.

Data Collection and Processing

Kaggle [13] is used to acquire CXR images of both normal and pneumonia. The dataset is organized into three folders: training, testing, and validation. Each folder contains two subfolders, namely Pneumonia and Normal. We only utilize the training and testing folders. There are 5,216 X-ray images in JPEG format. The normal CXR shows clean lungs with no areas of abnormal opacification in the CXR image. Pneumonia is characterized by a focal lobar consolidation in the CXR image. The collected images are of different sizes. To make the image dimensions uniform, the images are resized to 299 x 299. Next, the noise present in the images is cleared using histogram equalization. The obtained images are highly imbalanced, so undersampling is done to balance the data. Table I gives the complete analysis of the data used in this research.

PNEUMONIA AND NORMAL DATA ANALYSIS

Data	Lung Image	Train	Train	Test	Test
Normal		1341	1300	234	230
Pneumonia		3875	1300	390	230

Feature Extraction and Fusion

Feature extraction is an important step after processing. The relevant features are extracted from the images. Deep learning models like Inception and Xception are employed to retrieve these features. Next, the CCA technique is used to fuse the features obtained from the deep learning models. The architecture and workings of these techniques are detailed in this section.

Inception

GoogLeNet is a non-sequential CNN that makes use of the Inception network [14]. The explanation is based on the premise that layers become redundant when there are too many connections between them as a result of correlation. The Inception network is a standalone CNN. With 22 layers and a parallel workflow, the "Inception network" handles input. Multiple auxiliary classifiers are embedded in its intermediary layers. To increase the discrimination skills of the lower layers, supplementary classifiers are introduced. This network's support for convolutional and pooling methods extends to every layer. The use of filters with various widths inside the same layer is the network's defining feature. Consequently, the retrieved features are more distinct and available in different sizes [15]. The bottleneck layer, a 1×1 Convolutional Layer (CL), improves computing efficiency and reduces the CNN's parameter requirements. Along with 1×1 -CL, Inception networks also have 3×3 and 5×5 kernel convolutional filters. Before using 3×3 and 5×5 -CL, 1×1 layers are utilized to reduce parameter count at each level. Following 1×1 -CL, ReLU is used to deepen the network and increase non-linearity. Instead of employing Fully Connected Layers (FCL), this network employs the average pooling layer. The parameters are limited due to the absence of FCL. A minimum parameter does not prevent the Inception network from learning more complex features.

Xception

Xception is an improvement of the Inception architecture that uses depth-wise separable convolutions rather than standard Inception modules [16]. The additional inception layers were initially implemented by Xception, a deep CNN. These inception layers are built with depth-wise convolutional layers. The Xception network for extracting features is built around 36-CLs. The 36-CLs are split into 14 parts, each surrounded by linear residual connections except the first and last modules. The activation function used for the CLs is a nonlinear ReLU. The convolutional component consists of five sequential max-pooling layers. The first two sub-regions are supported by two CLs of 64 and 128 depth, respectively. In addition, the 1x1 convolution is used to permit the addition of the residual unit. L2 regularization is employed during the fine-tuned framework's implementation to lessen fitting challenges after each FCL. The Xception model produces 2,048 features.

Canonical Correlation Analysis

In this study, a single feature vector was generated by merging two types of deep features produced from separate networks employing distinct layers of deep features using the canonical correlation analysis (CCA) algorithm [17]. The fused feature is more discriminative than other input feature vectors. CCA is a widely used approach for analyzing correlations between groups of data.

Two matrices, $X \in \mathbb{R}^{(p \times n)}$ and $Y \in \mathbb{R}^{(q \times n)}$, are produced, where n represents the total samples when two algorithms are employed to retrieve the P and q -dimensional deep features. Following that, we extract a total of $(p+q)$ -dimensional features from each instance. The within-set covariance matrices of X and Y are designated by $S_{xx} = R^{(p \times p)}$ and $S_{yy} = R^{(q \times q)}$, respectively, while the between-set covariance matrix between X and Y is shown by $S_{xy} = R^{(p \times q)}$. The whole $(p+q) \times (p+q)$ covariance matrix, denoted as matrix S in Equation (1), contains information about the relationships between pairs of deep features.

$$S = \begin{pmatrix} \text{cov}(x) & \text{cov}(x,y) \\ \text{cov}(y,x) & \text{cov}(y) \end{pmatrix} = \begin{pmatrix} S_{xx} & S_{yx} \\ S_{xy} & S_{yy} \end{pmatrix} \quad [1]$$

However, it is difficult to discern the nature of the correlation between the sets of features from this matrix because their correlation may not follow a regular pattern [18]. CCA aims to optimize the pairwise correlation between two datasets and identify a linear transformation, $X^* = W_x^T X$ and $Y^* = W_y^T Y$.

$$\text{Corr}(X^*, Y^*) = \text{Corr}(X^*, Y^*) / (\text{Var}(X^*) \cdot \text{Var}(Y^*)) \quad [2]$$

Where

$$\text{Corr}(X^*, Y^*) = W_x^T S_{xy} W_y$$

$$\text{Var}(X^*) = W_x^T S_{xx} W_x$$

$$\text{Var}(Y^*) = W_y^T S_{yy} W_y$$

The Lagrange multiplier strategy increases the covariance between X^* and Y^* when $\text{Var}(X^*) = \text{Var}(Y^*) = 1$. X^* and Y^* are canonical variables in $\mathbb{R}^{(d \times n)}$. Furthermore, the eigenvalue equation can be solved using Equation (3) to obtain the linear transformation matrices W_x and W_y :

$$\{S_{xx}^{-1} S_{yy} S_{yy}^{-1} S_{yx} W_x = \Lambda^2 W_x, S_{yy}^{-1} S_{yx} S_{xx}^{-1} S_{xy} W_y = \Lambda^2 W_y\} \quad [3]$$

The eigenvectors are W_x and W_y , and the diagonal matrix containing the eigenvalues or squares of the canonical correlations is written as Λ^2 . The non-zero eigenvalues is represented as $d = \text{rank } S_{xy} \leq \min(n, p, q)$, then organized in descending order, $\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_d$. The transformation matrices W_x and W_y are derived from sorted eigenvectors corresponding to non-zero eigenvalues. Equation (4) defines the sample covariance matrix for the converted data, which has the following form:

$$S^* = \begin{bmatrix} 1 & 0 & \dots & 0 & \lambda_1 & 0 & \dots & 0 & 0 & 1 & 0 & \dots & 0 & \lambda_2 & 0 & \dots & 0 & \dots & 0 & 0 & 0 & \dots & 0 & \lambda_d & 0 & \dots & 0 & 0 & 1 & 0 & \dots & 0 & \lambda_d & 0 \\ 0 & 1 & \dots & 0 & 0 & \lambda_1 & 0 & \dots & 0 & 0 & 1 & 0 & \dots & 0 & 0 & \lambda_2 & 0 & \dots & 0 & \dots & 0 & 0 & 0 & \dots & 0 & 0 & 1 & 0 & \dots & 0 & 0 & \lambda_d & 0 \end{bmatrix} \quad [4]$$

The canonical variates in each data set are uncorrelated, as evidenced by the lower right and upper left identity matrices of the above matrix. The canonical variates have zero correlation with their respective indices. Equations (5) and (6) show the fusion equation as the concatenation or sum of the converted features (canonical variates X^* and Y^*). This enables the integration of deep features acquired from several CNN models.

$$Z_1 = (X^* \ Y^*) = (W_x^T X \ W_y^T Y) = (W_x \ 0 \ 0 \ W_y)^T (x \ y) \quad [5]$$

$$Z_2 = X^* + Y^* = W_x^T X + W_y^T Y = (W_x \ W_y)^T (x \ y) \quad [6]$$

Artificial Intelligence Model

The AI model is employed for the classification of pneumonia and normal CXR images. The workings of both models are detailed in this section using mathematical equations.

Support Vector Machine

Support vector machines (SVMs), a supervised ML technique, employ concepts from statistical learning and structural risk minimization to solve challenging classification tasks [19]. Using a training dataset, the SVM is designed to determine the optimum hyperplane for class distinction. The ideal hyperplane is the one with the greatest margin between the two categories, and a support vector is a collection of points that converge to it [20].

Consider a set of training vectors, represented as $y_i = \pm 1$, for data that allows linear separation x_i (where $i = 1, 2, \dots, n$), and classify them into two groups. The Equations (7) and (8) describe this method.

$$\frac{1}{2} \|w\|^2 \quad [7]$$

$$y_i ((w \cdot x_i) + b) \geq 1 \quad [8]$$

In this scenario, the coefficient vector w defines the hyperplane's orientation in the feature space, while b represents its offset from the origin. Equation (9) defines a cost function that uses the Lagrange multiplier:

$$L = \frac{1}{2} \|w\|^2 - \sum_{i=1}^n \lambda_i ((y_i (w \cdot x_i) + b) - 1) \quad [9]$$

The Lagrange multiplier is denoted by λ_i . Given the difficulties of linear data classification, it is reasonable to convert a nonlinear space to a linear one to obtain optimal class separation. To address misclassification, we introduce $v(0,1)$ and employ slack variables ξ_i ($\xi_i \geq 0$) to adjust the constraints.

$$y_i (w \cdot x_i + b) \geq 1 - \xi_i \quad [10]$$

$$L = \frac{1}{2} \|w\|^2 - \frac{1}{v_n} \sum_{i=1}^n \xi_i \quad [11]$$

We used the sigmoid function (SIG) which is defined in Equation (12):

$$\text{SIG}: K(x_i, x_j) = \tanh(\gamma X_i^T X_j + r) \quad [12]$$

Where the γ term determines the kernel's width and a bias term is manually input into the functions in order to enhance SVM's accuracy.

Bayesian Logistic Regression

The pneumonia was diagnosed using Bayesian logistic regression (BLR). The correlations between the two sets of data can be used to build a logistic regression model [21]. The next stage is to employ a Bayesian function that considers the reactions and behavior of the effective components using a prior probability function [22]. To create a Bayesian function, follow the three steps outlined below:

1. Calculate the parameter's prior probability.
2. Analyze the data to determine the likelihood function.
3. Put the parameters into a posterior distribution.

The logistic function extracts the posterior probability function for samples belonging to a specific class from a training dataset $x = (x_1, x_2, \dots, x_n)$, where x represents independent factors and $y = (y_1, y_2, \dots, y_n)$ is a dependent variable (pneumonia and normal).

$$P(\text{Class} | x_1, x_2, \dots, x_n) = \frac{1}{(1 + \exp^{(b + w_0 + \sum_{i=1}^n w_i f(x_i))})} \quad [13]$$

where x_i denotes the effective factors, c represents the previous log odds ratio ($c = \log P(\text{class}=0)/P(\text{class}=1)$), and b represents the bias. The i -th factors of x_i are used to compute the $f(x_i)$ function, with w_0 and w_i acting as weights trained on the training data. For binary variables, this is accomplished by dividing $\log P(x_i | \text{class}=0)/P(x_i | \text{class}=1)$. The weights of the Bayesian logistic regression model are determined a priori using a univariate Gaussian function.

$$P(W | \sigma_i) = N(0, \sigma_i) = \frac{1}{\sqrt{2\pi\sigma_i}} \exp^{(-(w^2)/2\sigma_i)} \quad [14]$$

where σ_i and 0 are the data variance, and average, respectively.

Result and Discussion

For pneumonia detection, the normal and pneumonia-affected CXR images are taken and processed. The features are extracted using Inception and Xception networks. Then both sets of features are fused using the CCA algorithm. The individual and fused features are given to the SVM and BLR models for classification. The outcomes of both models on various features are detailed in this section. Both models are validated using performance measures like accuracy, specificity, recall, precision, and F1 score [23, 24].

Outcome of the SVM Model

The features from Inception, Xception, and the CCA technique are given to the SVM model. The confusion matrix of the SVM on three features is given in Figure 1. The elements of the confusion matrix help calculate the performance measures.

a) Inception Features

b) Xception Features

c) Fused Features

Confusion matrix of SVM model on various features.

The SVM model gives an accuracy of 92.39%, specificity of 91.74%, recall of 93.04%, precision of 91.85%, and F1-score of 92.44% on Inception features. For Xception features, the model gives an accuracy of 94.13%, specificity of 93.89%, recall of 94.37%, precision of 93.97%, and F1-score of 94.17%. With the fused features, the SVM attains an accuracy of 97.61%, specificity of 96.97%, recall of 98.25%, precision of 96.98%, and F1-score of 97.61%. By comparing all the metrics, the fused features help the SVM model attain better results in pneumonia detection. Table II gives the performance values of the SVM model on pneumonia detection using various features. The values in the table are given in percentage. Figure 2 provides the comparison plot of feature extraction techniques on the SVM model.

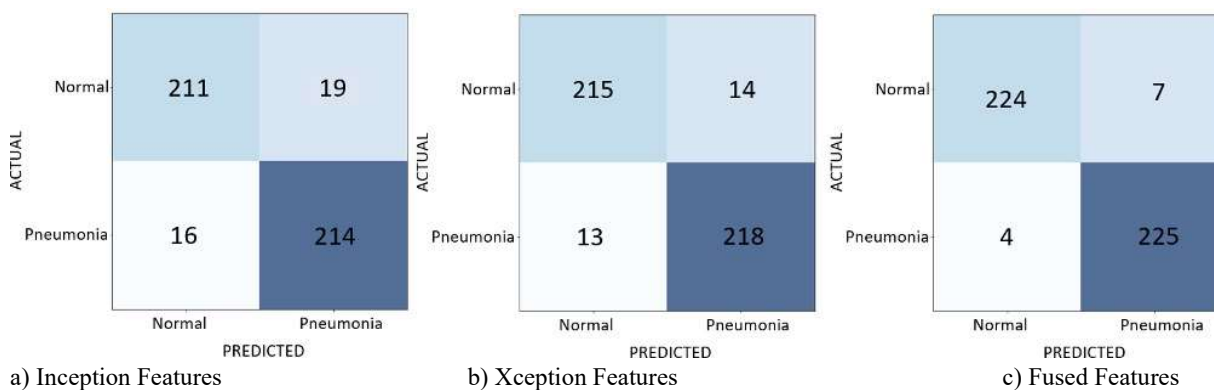
SVM PERFORMANCE COMPARISON USING VARIOUS FEATURES

Features	Accuracy	Specificity	Recall	Precision	F1-Score
Inception	92.39	91.74	93.04	91.85	92.44
Xception	94.13	93.89	94.37	93.97	94.17
Fused Features	97.61	96.97	98.25	96.98	97.61

Performance analysis of the SVM model using various features.

Outcome of the BLR Model

The BLR model is then taken and validated. The confusion matrix of the BLR model on Inception, Xception, and fused features is given in Figure 3.

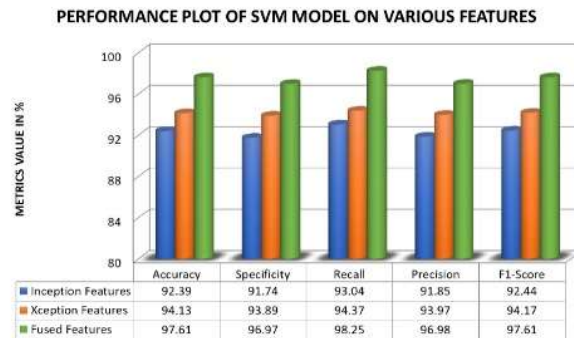


Confusion matrix of BLR model on various features.

From this confusion matrix, the performance metrics are calculated and given in Table III. The BLR model gives the highest accuracy of 98.91% when applying fused features, and the model gives 94.35% and 95.65% on Inception and Xception features, respectively. Next, the specificity of the BLR gives a maximum value of 99.13% on fused features, with the lowest specificity attained by Inception features. For recall, the BLR gives 94.78%, 96.52%, and 98.70% on Inception, Xception, and fused features, respectively. Finally, the model gives the highest precision and F1 score of 99.13% and 98.91% on fused features. The minimum precision and F1 score are given by the Inception model. Figure 4 provides the comparison plot of feature extraction techniques on the BLR model.

BLR PERFORMANCE COMPARISON USING VARIOUS FEATURES

Features	Accuracy	Specificity	Recall	Precision	F1-Score
Inception	92.39	91.74	93.04	91.85	92.44
Xception	94.13	93.89	94.37	93.97	94.17
Fused Features	97.61	96.97	98.25	96.98	97.61



Performance analysis of the BLR model using various features.

Conclusion

Pneumonia is one of the leading causes of death globally. And it is challenging to diagnose pneumonia simply based on CXR images. The goal of this study is to make pneumonia detection easier for both experts and beginners. To achieve this, CXR images of normal and pneumonia cases are collected and processed. Features are extracted from the processed images using Xception and Inception networks. The extracted features are then fused using the CCA method. All three sets of features (Xception, Inception, and fused) are given to the SVM and BLR models for classification. The BLR model with fused features gives better performance in pneumonia detection, achieving an accuracy, specificity, recall, precision, and F1-score of 98.91%, 99.13%, 98.70%, 99.13%, and 98.91%, respectively. Next, the SVM with fused features gives better performance. It achieves an accuracy of 97.61%, specificity of 96.97%, recall of 98.25%, precision of 96.98%, and F1-score of 97.61%. The result shows that the fused feature helps to enhance the AI model's accuracy in pneumonia detection. The execution time of the model is not analyzed in this research. Execution time is very important when deploying the model in hardware. In future work, the analysis of execution time will be done, and the best model will be deployed in hardware using FPGA (Field-Programmable Gate Array).

References

- Long, Matthew E., Rama K. Mallampalli, and Jeffrey C. Horowitz. "Pathogenesis of pneumonia and acute lung injury." *Clinical Science* 136, no. 10 (2022): 747-769.
- Ferkol, Thomas, and Dean Schraufnagel. "The global burden of respiratory disease." *Annals of the American Thoracic Society* 11, no. 3 (2014): 404-406.
- Celentano, David D., Elizabeth Platz, and Shruti H. Mehta. "The centennial of the Department of Epidemiology at Johns Hopkins Bloomberg School of Public Health: a century of epidemiologic discovery and education." *American journal of epidemiology* 188, no. 12 (2019): 2043-2048.
- Kareem, Amer, Haiming Liu, and Paul Sant. "Review on pneumonia image detection: A machine learning approach." *Human-Centric Intelligent Systems* 2, no. 1 (2022): 31-43.
- Vieira, Pablo, Orrana Sousa, Deborah Magalhães, Ricardo Rabêlo, and Romuere Silva. "Detecting pulmonary diseases using deep features in X-ray images." *Pattern Recognition* 119 (2021): 108081.
- Ojetunmibi, T., P. O. Asagba, and U. A. Okengwu. "Pneumonia disease detection and classification system using naive Bayesian technique." *Scientia Africana* 22, no. 1 (2023): 97-114.
- Çelik, Ahmet, and Semih Demirel. "Enhanced Pneumonia Diagnosis Using Chest X-Ray Image Features and Multilayer Perceptron and k-NN Machine Learning Algorithms." *Traitement du Signal* 40, no. 3 (2023): 1015.
- Bahuguna, Aman, Deepak Yadav, Apurbalal Senapati, and Baidya Nath Saha. "k NN-SVM with Deep Features for COVID-19 Pneumonia Detection from Chest X-ray." In *International Conference on Mathematics and Computing*, pp. 103-115. Singapore: Springer Nature Singapore, 2022.
- Goyal, Shimpy, and Rajiv Singh. "Detection and classification of lung diseases for pneumonia and Covid-19 using machine and deep learning techniques." *Journal of Ambient Intelligence and Humanized Computing* 14, no. 4 (2023): 3239-3259.
- Mabrouk, Alhassan, Rebeca P. Diaz Redondo, Abdelghani Dahou, Mohamed Abd Elaziz, and Mohammed Kayed. "Pneumonia detection on chest X-ray images using ensemble of deep convolutional neural networks." *Applied Sciences* 12, no. 13 (2022): 6448.
- Praskatama, Vincentius, Christy Atika Sari, Eko Hari Rachmawanto, and Noorayisahbe Mohd Yaacob.

"Pneumonia Prediction Using Convolutional Neural Network." Jurnal Teknik Informatika (Jutif) 4, no. 5 (2023): 1217-1226.

Bhatt, Harsh, and Manan Shah. "A Convolutional Neural Network ensemble model for Pneumonia Detection using chest X-ray images." Healthcare Analytics 3 (2023): 100176.

<https://www.kaggle.com/datasets/paultimothymooney/chest-xray-pneumonia>

Szegedy, Christian, Vincent Vanhoucke, Sergey Ioffe, Jon Shlens, and Zbigniew Wojna. "Rethinking the inception architecture for computer vision." In Proceedings of the IEEE conference on computer vision and pattern recognition, pp. 2818-2826. 2016.

Szegedy, Christian, Sergey Ioffe, Vincent Vanhoucke, and Alexander Alemi. "Inception-v4, inception-resnet and the impact of residual connections on learning." In Proceedings of the AAAI conference on artificial intelligence, vol. 31, no. 1. 2017.

Chollet, François. "Xception: Deep learning with depthwise separable convolutions." In Proceedings of the IEEE conference on computer vision and pattern recognition, pp. 1251-1258. 2017.

Sun, Quan-Sen, Sheng-Gen Zeng, Yan Liu, Pheng-Ann Heng, and De-Shen Xia. "A new method of feature fusion and its application in image recognition." Pattern Recognition 38, no. 12 (2005): 2437-2448.

Krzanowski, Wojtek. Principles of multivariate analysis. Vol. 23. OUP Oxford, 2000.

Kecman, V. "Basics of machine learning by support vector machines." In Real World Applications of Computational Intelligence, pp. 49-103. Berlin, Heidelberg: Springer Berlin Heidelberg, 2005.

Çevik, Abdulkadir, Ahmet Emin Kurtoğlu, Mahmut Bilgehan, Mehmet Eren Gülşan, and Hasan M. Albegmpri. "Support vector machines in structural engineering: a review." Journal of Civil Engineering and Management 21, no. 3 (2015): 261-281.

Hilbe, Joseph M. Logistic regression models. Chapman and hall/CRC, 2009.

O'brien, Sean M., and David B. Dunson. "Bayesian multivariate logistic regression." Biometrics 60, no. 3 (2004): 739-746.

Sokolova, Marina, and Guy Lapalme. "A systematic analysis of performance measures for classification tasks." Information processing & management 45, no. 4 (2009): 427-437.

Tharwat, Alaa. "Classification assessment methods." Applied computing and informatics 17, no. 1 (2021): 168-192.